

# Jesse Eaton

Machine Learning Scientist

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## EDUCATION

### Carnegie Mellon University

M.S. Computational Biology, School of Computer Science, GPA: 3.91

December 2017

### Tufts University

B.S. Biomedical Engineering, GPA: 3.45

May 2015

## SKILLS

**Languages:** Python, C++, C, Golang

**Machine Learning:** Sklearn, XGBoost, Pytorch, Flyte

**Math:** Algorithms, Probability, Statistics, Regression

**Other:** Genomics, Gcloud

## EXPERIENCE

### Senior Machine Learning Scientist, Freenome

September 2019 - Present

- Developed core machine learning model increasing classification performance of colorectal cancer detection to industry high of 0.9 sensitivity at 0.9 specificity
- Designed important features with high signal to noise in genomics data
- Promoted iterations of important models by developing framework for model comparison
- Streamlined user model reports by redesigned reporting and model diagnostic infrastructure
- Managed ML science intern leading to development of robust kmer model pipeline

### Machine Learning Research Engineer, Qeexo

February 2018 - April 2019

- Generated multiple experimental company products by fusing sensor data with efficient machine learning classifiers <https://www.youtube.com/watch?v=1S6irWy8G20>
- Compressed gradient boosting classifier to 20 kB size for highly time/space/energy constrained environments achieving < 5ms classification time
- Increased customer awareness by demoing projects at Consumer Electronics Show 2019

### Software Systems Engineer, MITRE

September 2015 - August 2016

- Built web based electronic medical validation tool for Health Services Department as main engineer using Amazon Elastic Compute Cloud (AWS)

## PUBLICATIONS

**Jesse Eaton**, Jingyi Wang, Russell Schwartz, "Deconvolution and phylogeny inference of structural variations in tumor genomic samples." *Bioinformatics*, Volume 34, Issue 13, 01 July 2018, Pages i357–i365

Yifeng Tao, Ashok Rajaraman, Xiaoyue Cui, Ziyi Cui, **Jesse Eaton**, Hannah Kim, Jian Ma, Russell Schwartz, "Improving personalized prediction of cancer prognoses with clonal evolution models." *bioRxiv* 761510

## LEADERSHIP AND AWARDS

**Culture Leader**, Freenome, Jan 2022. Nominated as one of 10 culture leaders for exemplifying values

**Patent for signal discovery**, Freenome, April 2020. Discovered novel miRNA signal for colon cancer